

REMARKS

In the Advisory Action mailed January 15, 2003, the rejection of claims 1-5 under 35 U.S.C. §101 and §112 is maintained for the reasons set forth in the Final Rejection (Paper No. 15). The Examiner maintains that Applicants' Amendment and Response filed February 19, 2002, was not persuasive because the copies of SEQ ID No. 6 (SR-p70) of the instant application and SEQ ID No. 1 of WO 99/66946 (p73), attached to the Response to show that the polypeptides are identical, were not submitted, and that in any event, the copies of the sequences, as well as the Br. J. Cancer 2001 reference also submitted with Applicants' response, would not have been considered because Applicants had not shown good and sufficient reasons why the documents were not earlier presented.

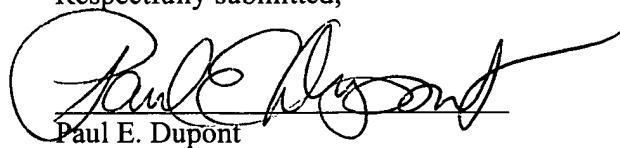
Applicants hereby request that the sequences, copies of which are resubmitted herewith, the Br. J. Cancer 2001 reference, and the Response filed February 19, 2002, be fully considered. It is submitted that the rejection under 35 U.S.C. §101 and §112 is fully met by the previous response and supporting documents, and accordingly, reconsideration and withdrawal of said rejection are respectfully requested.

Claim 3 remains rejected under 35 U.S.C. §102 for the reasons of record, namely, that subject matter of the Dequiedt et al reference falls within the scope of claim 3. The rejection is believed overcome by the foregoing amendment of claim 3 to more particularly describe the amino acid sequences of SEQ ID No. 2 and 6 between residues 110 and 310 and the amino acid sequence of SEQ ID No. 8 between residue 60 and residue 260. The Dequiedt et al reference does not disclose any sequence falling within the scope of claim 3 as amended and hence does not anticipate Applicants' claims. Accordingly, the rejection should be withdrawn.

There being no remaining issues this application is believed in condition for allowance and such action is earnestly solicited.

Respectfully submitted,

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Paul E. Dupont

Registration No. 27,438

Sanofi-Synthelabo Inc.
Patent Department
9 Great Valley Parkway
P.O. Box 3026
Malvern, PA 19355
Tel.: (610) 889-6338
Fax: (610) 889-8799

Version With Markings to Show Changes Made

In the Claims:

Claim 3 has been amended as follows:

3. (Twice amended) A polypeptide according to Claim 1 comprising a an amino acid sequence lying between:

— residue 110 and residue 310 of selected from the group consisting of SEQ ID No. 2 or 6; from residue 110 to residue 310, SEQ ID No. 6 from residue 110 to residue 310, and
— residue 60 and residue 260 of SEQ ID No. 8 from residue 60 to residue 260.



SEQ ID No. 6 of Serial No. 09/125,005 (SR-p70)

<400> 6

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
1 5 10 15
His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
20 25 30
Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser
35 40 45
Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
50 55 60
Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
65 70 75 80
Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His
85 90 95
Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
100 105 110
Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
115 120 125
Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
130 135 140
Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
145 150 155 160
Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg
165 170 175
Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
180 185 190
Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser
195 200 205
Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln
210 215 220
Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr
225 230 235 240
Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe
245 250 255
Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu
260 265 270
Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg
275 280 285
Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala
290 295 300
Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala
305 310 315 320
Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala
325 330 335
Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu
340 345 350
Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu
355 360 365
Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro
370 375 380
Leu Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Ser
385 390 395 400
His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys
405 410 415
Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly
420 425 430
Gln Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val
435 440 445
Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly
450 455 460
Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His
465 470 475 480
Cys Thr Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe
485 490 495
Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln
500 505 510
Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu
515 520 525
Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly
530 535 540
Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu
545 550 555 560
Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu
565 570 575
Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His
580 585 590
Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Pro Asp Glu
595 600 605
Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln
610 615 620
Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His
625 630 635

SEQ ID No. 1 of WO 99/66946 (p73)

<400> 1
 Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
 1 5 10 15
 His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
 20 25 30
 Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser
 35 40 45
 Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
 50 55 60
 Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
 65 70 75 80
 Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His
 85 90 95
 Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
 100 105 110
 Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
 115 120 125
 Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
 130 135 140
 Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
 145 150 155 160
 Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg
 165 170 175
 Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
 180 185 190
 Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser
 195 200 205
 Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln
 210 215 220
 Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr
 225 230 235 240
 Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe
 245 250 255
 Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu
 260 265 270
 Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg
 275 280 285
 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala
 290 295 300
 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala
 305 310 315 320
 Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala
 325 330 335
 Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu
 340 345 350
 Asp Thr Tyr Tyr Leu Gin Val Arg Gly Arg Glu Asn Phe Glu Ile Leu
 355 360 365
 Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro
 370 375 380
 Leu Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Ser
 385 390 395 400
 His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys
 405 410 415
 Val His Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly
 420 425 430
 Gln Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val
 435 440 445
 Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly
 450 455 460
 Glu Met Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His
 465 470 475 480
 Cys Thr Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe
 485 490 495
 Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln
 500 505 510
 Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu
 515 520 525
 Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly
 530 535 540
 Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu
 545 550 555 560
 Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu
 565 570 575
 Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His
 580 585 590
 Thr Ile Thr Ile Pro Asn Arg Gly Pro Gly Gly Pro Asp Glu
 595 600 605
 Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln
 610 615 620
 Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His
 625 630 635